

SEQUENCE LISTING

<110> Conklin, Darrell C.
 Gao, Zeren
 Lofton-Day, Catherine E.
 Whitmore, Theodore E.

<120> SECRETED ALPHA-HELICAL PROTEIN ZLMDA24

<130> 00-94

<150> US 60/242,023

<151> 2000-10-20

<160> 25

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1041

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (205)...(966)

<400> 1

ctgagaacac cagaggactg gcagttggga gcctgatgga ggacaagtag ggcctcgagg	60
acaggtgcgt gacagaagca caggaaaaaa aagaaaaatg aagaaataaa aacacgagtt	120
catcagtaaa gaggtaccct ggcagcataa atattatgat aagctaaaag ctggaatcat	180
ctggaaaaat aaataagact cctc atg tcc ttt tcg gtc cat aac cag aag	231
Met Ser Phe Ser Val His Asn Gln Lys	
1 5	

ggc agc aaa agg cct ttg cca ctg gaa cct ctt ctt ttt ctc caa gtc	279
Gly Ser Lys Arg Pro Leu Pro Leu Glu Pro Leu Leu Phe Leu Gln Val	
10 15 20 25	

cca cgt agc aat tac ctg cac ttt caa gaa gag aaa caa cga cta cac	327
---	-----

Pro	Arg	Ser	Asn	Tyr	Leu	His	Phe	Gln	Glu	Glu	Lys	Gln	Arg	Leu	His	
				30					35					40		
cta	aag	aaa	ttc	ctt	ctt	gat	agg	atg	ttt	cta	gtg	gcc	aag	ata	caa	375
Leu	Lys	Lys	Phe	Leu	Leu	Asp	Arg	Met	Phe	Leu	Val	Ala	Lys	Ile	Gln	
			45					50					55			
gca	aat	gta	gaa	aga	aaa	gat	gtt	gct	gac	tac	tat	gaa	caa	atg	ttt	423
Ala	Asn	Val	Glu	Arg	Lys	Asp	Val	Ala	Asp	Tyr	Tyr	Glu	Gln	Met	Phe	
		60					65					70				
cag	tca	gtt	ttg	aaa	cat	cac	cta	gga	gaa	gca	gtg	aca	gga	ttg	ctg	471
Gln	Ser	Val	Leu	Lys	His	His	Leu	Gly	Glu	Ala	Val	Thr	Gly	Leu	Leu	
	75					80					85					
ctc	atc	tat	ccc	act	tcc	att	ctg	cat	atc	ctc	gag	tcc	tcc	agc	gac	519
Leu	Ile	Tyr	Pro	Thr	Ser	Ile	Leu	His	Ile	Leu	Glu	Ser	Ser	Ser	Asp	
90					95				100						105	
act	ctc	tac	aaa	gtt	ctt	tta	gat	tat	att	ggc	cat	gtc	aaa	gat	gaa	567
Thr	Leu	Tyr	Lys	Val	Leu	Leu	Asp	Tyr	Ile	Gly	His	Val	Lys	Asp	Glu	
			110						115					120		
aca	gta	ttt	ttt	att	caa	caa	atg	aaa	att	ata	gtc	att	tct	cat	aac	615
Thr	Val	Phe	Phe	Ile	Gln	Gln	Met	Lys	Ile	Ile	Val	Ile	Ser	His	Asn	
		125						130					135			
att	cca	atg	agg	ctt	ttt	atg	caa	tgg	cat	gtt	tca	gtg	ata	aaa	gtt	663
Ile	Pro	Met	Arg	Leu	Phe	Met	Gln	Trp	His	Val	Ser	Val	Ile	Lys	Val	
	140						145					150				
cca	gtt	atg	tat	ctc	gac	gat	gtg	aca	cag	tca	cag	tcc	cta	aag	gag	711
Pro	Val	Met	Tyr	Leu	Asp	Asp	Val	Thr	Gln	Ser	Gln	Ser	Leu	Lys	Glu	
	155					160					165					
gtc	atc	aca	gat	ttt	ctc	aca	caa	act	cat	aaa	ctg	tca	ctc	tac	ctt	759
Val	Ile	Thr	Asp	Phe	Leu	Thr	Gln	Thr	His	Lys	Leu	Ser	Leu	Tyr	Leu	
170					175					180					185	
tgc	cag	act	atg	aaa	gta	ggc	act	aaa	gga	cca	ggc	gat	aac	tta	cac	807
Cys	Gln	Thr	Met	Lys	Val	Gly	Thr	Lys	Gly	Pro	Gly	Asp	Asn	Leu	His	
			190						195					200		

caa gtt gca cct gac cta ctc ctc cca gaa caa atc ata aag tac ttg 855
 Gln Val Ala Pro Asp Leu Leu Leu Pro Glu Gln Ile Ile Lys Tyr Leu
 205 210 215

tgc aaa tcc gaa gaa ttc atg gac ccg gca aca ttt ata aac atg tat 903
 Cys Lys Ser Glu Glu Phe Met Asp Pro Ala Thr Phe Ile Asn Met Tyr
 220 225 230

aat aga ccc ata cac atc act ctg gat tct gag gtg gta tgg cct gct 951
 Asn Arg Pro Ile His Ile Thr Leu Asp Ser Glu Val Val Trp Pro Ala
 235 240 245

cct tca cgt ttc tag gattgagagg gataatgtgc ccatgtctct taaggagttt 1006
 Pro Ser Arg Phe *
 250

gtgctactta aataaaaaaaaa acattttttaa agtta 1041

<210> 2

<211> 253

<212> PRT

<213> Human

<400> 2

Met	Ser	Phe	Ser	Val	His	Asn	Gln	Lys	Gly	Ser	Lys	Arg	Pro	Leu	Pro
1				5					10					15	
Leu	Glu	Pro	Leu	Leu	Phe	Leu	Gln	Val	Pro	Arg	Ser	Asn	Tyr	Leu	His
			20				25						30		
Phe	Gln	Glu	Glu	Lys	Gln	Arg	Leu	His	Leu	Lys	Lys	Phe	Leu	Leu	Asp
			35				40					45			
Arg	Met	Phe	Leu	Val	Ala	Lys	Ile	Gln	Ala	Asn	Val	Glu	Arg	Lys	Asp
	50					55				60					
Val	Ala	Asp	Tyr	Tyr	Glu	Gln	Met	Phe	Gln	Ser	Val	Leu	Lys	His	His
65					70				75					80	
Leu	Gly	Glu	Ala	Val	Thr	Gly	Leu	Leu	Leu	Ile	Tyr	Pro	Thr	Ser	Ile
				85				90						95	
Leu	His	Ile	Leu	Glu	Ser	Ser	Ser	Asp	Thr	Leu	Tyr	Lys	Val	Leu	Leu
			100					105					110		
Asp	Tyr	Ile	Gly	His	Val	Lys	Asp	Glu	Thr	Val	Phe	Phe	Ile	Gln	Gln
		115				120						125			
Met	Lys	Ile	Ile	Val	Ile	Ser	His	Asn	Ile	Pro	Met	Arg	Leu	Phe	Met
	130					135					140				

Gln Trp His Val Ser Val Ile Lys Val Pro Val Met Tyr Leu Asp Asp
 145 150 155 160
 Val Thr Gln Ser Gln Ser Leu Lys Glu Val Ile Thr Asp Phe Leu Thr
 165 170 175
 Gln Thr His Lys Leu Ser Leu Tyr Leu Cys Gln Thr Met Lys Val Gly
 180 185 190
 Thr Lys Gly Pro Gly Asp Asn Leu His Gln Val Ala Pro Asp Leu Leu
 195 200 205
 Leu Pro Glu Gln Ile Ile Lys Tyr Leu Cys Lys Ser Glu Glu Phe Met
 210 215 220
 Asp Pro Ala Thr Phe Ile Asn Met Tyr Asn Arg Pro Ile His Ile Thr
 225 230 235 240
 Leu Asp Ser Glu Val Val Trp Pro Ala Pro Ser Arg Phe
 245 250

<210> 3
 <211> 1056
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (106)...(867)

<400> 3

gcagaggtca agccaagagg acctcagacc tcaaagacag aaataaaaaat aagaattcac 60
 taccattgag acttgtaatc atctaaaaaa gaaataagat tcatc atg tct ttc atg 117
 Met Ser Phe Met
 1

gtc cat aat cgg aag ggc agc aaa aag caa ttt caa gtg gat cct ctt 165
 Val His Asn Arg Lys Gly Ser Lys Lys Gln Phe Gln Val Asp Pro Leu
 5 10 15 20

ctt ctg ccc aag gtt cct cgt acc aat tac ctg cac ctt cag gaa gag 213
 Leu Leu Pro Lys Val Pro Arg Thr Asn Tyr Leu His Leu Gln Glu Glu
 25 30 35

aag cac aga cta cag cta aag aaa ttc ctc ctt cac agg atg ttt cta 261
 Lys His Arg Leu Gln Leu Lys Lys Phe Leu Leu His Arg Met Phe Leu
 40 45 50

gtg ggc tac ata caa ggc aac acg gag aaa aag gac atc tct gag tac 309

att atc aag tat tta tgc aaa gct gaa gaa ttc atg gac cca gcg tct 789
Ile Ile Lys Tyr Leu Cys Lys Ala Glu Glu Phe Met Asp Pro Ala Ser
215 220 225

ttc ttg agc atg tat aac aga ccc ata cac gtt acc ctg gat tcc gat 837
 Phe Leu Ser Met Tyr Asn Arg Pro Ile His Val Thr Leu Asp Ser Asp
 230 235 240

att gtg tgg cca gct cct tcc cgt ttc tag aatggggaga gttgatttg 887
 Ile Val Trp Pro Ala Pro Ser Arg Phe *
 245 250

agaggatgtc tacaacattc agaagcattg aagatggcac cagagcagga gggtgaaaga 947
 acgcatgttc agccagggcat agaacaggag ccaggaaggg gacaacacca taaattcctg 1007
 aatttctttg tgtttttaggc actaaacata ataaatttct taagactga 1056

<210> 4

<211> 253

<212> PRT

<213> Mus musculus

<400> 4

Met Ser Phe Met Val His Asn Arg Lys Gly Ser Lys Lys Gln Phe Gln
 1 5 10 15
 Val Asp Pro Leu Leu Leu Pro Lys Val Pro Arg Thr Asn Tyr Leu His
 20 25 30
 Leu Gln Glu Glu Lys His Arg Leu Gln Leu Lys Lys Phe Leu Leu His
 35 40 45
 Arg Met Phe Leu Val Gly Tyr Ile Gln Gly Asn Thr Glu Lys Lys Asp
 50 55 60
 Ile Ser Glu Tyr Tyr Glu Gln Leu Phe Gln Ser Ile Leu Lys His His
 65 70 75 80
 Leu Gly Glu Ser Val Thr Gly Leu Met Leu Val Tyr Pro Ser Thr Phe
 85 90 95
 Leu His Ile Leu Glu Ser Ser Asn Gly Thr Leu Phe Arg Ile Leu Leu
 100 105 110
 Asp Tyr Val Ala His Glu Lys Ser Glu Thr Glu Phe Met Leu Gln Asn
 115 120 125
 Met Lys Ile Val Val Ala Ser His Asn Ile Pro Thr Arg Leu Phe Met
 130 135 140
 Gln Trp His Ile Ser Ala Ile Lys Val Pro Val Leu Tyr Leu Asp Asp
 145 150 155 160
 Glu Ser Gln Ser Pro Ser Ile Glu Glu Val Thr Thr Glu Phe Leu Thr
 165 170 175
 Met Thr His Lys Leu Ala Leu Gln Leu Tyr Lys Thr Val Lys Leu Gly
 180 185 190

Ala Lys Gly Pro Gly Asp Asn Leu His Gln Leu Ala Pro Glu Leu Ile
 195 200 205
 Leu Pro Glu Gln Ile Ile Lys Tyr Leu Cys Lys Ala Glu Glu Phe Met
 210 215 220
 Asp Pro Ala Ser Phe Leu Ser Met Tyr Asn Arg Pro Ile His Val Thr
 225 230 235 240
 Leu Asp Ser Asp Ile Val Trp Pro Ala Pro Ser Arg Phe
 245 250

<210> 5
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate polynucleotide sequence of human z1mda24
 shown in SEQ ID NO:2

<221> misc_feature
 <222> (1)...(759)
 <223> n = A,T,C or G

<400> 5
 atgwsnttyw sngtncayaa ycaraarggn wsnaarmgnc cnytnccnyt ngarccnytn 60
 yntttyytnc argtnccnmg nwsnaaytay ytncayttyc argargaraa rcarmgnytn 120
 cayytnaara arttyytnyt ngaymgntatg ttyytngtng cnaarathca rgcnaaygtn 180
 garmgnaarg aygtngcnga ytaytaygar caratgttyc arwsngtnyt naarcaycay 240
 ytnggngarg cngtnacngg nytnytnytn athtayccna cnwsnathyt ncayathytn 300
 garwsnwnw sngayacnyt ntayaargtn ytnytnngayt ayathggncay ygtnaargay 360
 garacngtnt tyttyathca rcaratgaar athathgtna thwsncayaa yathccnatg 420
 mgnytnttya tgcartggca ygtnwsngtn athaargtnw sngtnatgta yytnngaygay 480
 gtnacncarw snrcarwsnyt naargargtn athacngayt tyytnacnca racncayaar 540
 ytnwsnytnnt ayytntgyca racnatgaar gtnggnacna arggnccngg ngayaayytn 600
 caycargtng cncngayyt nytnytnccn garcaratha thaartayyt ntgyaarwsn 660
 gargarttya tggayccngc nactnttyath aayatgtaya aymgnccnat hcayathacn 720
 ytngaywsng argtngtntg gccngcncn wsnmgntty 759

<210> 6
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of mouse
z1mda24 shown in SEQ ID NO:4

<221> misc_feature

<222> (1)...(759)

<223> n = A,T,C or G

<400> 6

atgwsnttya tggtncaayaa ymгнаaarggn wsnaaraarc arttycargt ngayccnytn	60
ytnytnccna argtnccnmg nacnaaytay ytncayytn argargaraa rcaymgnytn	120
carytnaara arttyytnyt ncaymgnatg ttyytngtn gntayathca rggnaayacn	180
garaaraarg ayathwsnga rtaytaygar carytnntyc arwsnathyt naarcaycay	240
ytngnggarw sngtnacngg nytnatgytn gntayccnw snacnttyt ncayathytn	300
garwsnwsna aygnnacnynt nttymgnath ytnytngayt aygtngcnca ygaraarwsn	360
garacngart tyatgytnca raayatgaar athgtngtn cwnsncaayaa yathccnacn	420
mgnynttya tgcartggca yathwsngcn athaargtn cngtnytnta yytngaygay	480
garwsncarw snccwnsnat hgargargtn acnacngart tyytnacnat gacncayaar	540
ytngcnytn arytnayaa racngtnaar ytngngcna arggnccngg ngayaaytn	600
caycarytn cncngaryt nathytnccn garcaratha thaartayt ntgyaargcn	660
gargarttya tggayccngc nwsnttytn wsnatgtaya aymgnccnat hcaygtnacn	720
ytngaywsng ayathgtntg gccngcncn wsnmgntty	759

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29714

<400> 7

aacagaccca tacacgttac cctgg	25
-----------------------------	----

<210> 8

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29984

<400> 8

tcttgcccc ttctggctc ctg	23
-------------------------	----

<210> 9
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC21195

<400> 9
 gaggagacca taacccccga cag 23

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC21196

<400> 10
 catagctccc accacacgat ttt 23

<210> 11
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC14063

<400> 11
 caccagacat aatagctgac agact 25

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC17574

<400> 12

ggtrttgctc agcatgcaca c 21

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC17600

<400> 13

catgtaggcc atgaggtcca ccac 24

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28587

<400> 14

gattgctgct catctatccc actt 24

<210> 15

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28591

<400> 15

tggtgtaagt tatcgctgg tcc 23

<210> 16

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29567

<400> 16
cctcccagaa caaatcat 18

<210> 17
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29568

<400> 17
accacctcag aatccaga 18

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Glu-Glu (CEE) Tag amino acid sequence

<400> 18
Glu Tyr Met Pro Met Glu
1 5

<210> 19
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Sequence ZC29055

<400> 19
cgcggatccc gatgtccttt tcggtccata a 31

<210> 20
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide Sequence ZC29056

<400> 20

tgctctagag cgaaacgtga aggagcaggc cata

34

<210> 21

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Sequence ZC447

<400> 21

taacaatttc acacagg

17

<210> 22

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Sequence ZC976

<400> 22

cgttgtaaaa cgacggcc

18

<210> 23

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> Representative zlmda24 polypeptide containing
C-terminal Glu-Glu (CEE) tag

<400> 23

Met	Ser	Phe	Ser	Val	His	Asn	Gln	Lys	Gly	Ser	Lys	Arg	Pro	Leu	Pro
1				5					10					15	
Leu	Glu	Pro	Leu	Leu	Phe	Leu	Gln	Val	Pro	Arg	Ser	Asn	Tyr	Leu	His
			20					25					30		
Phe	Gln	Glu	Glu	Lys	Gln	Arg	Leu	His	Leu	Lys	Lys	Phe	Leu	Leu	Asp
		35					40						45		

```

Arg Met Phe Leu Val Ala Lys Ile Gln Ala Asn Val Glu Arg Lys Asp
 50          55          60
Val Ala Asp Tyr Tyr Glu Gln Met Phe Gln Ser Val Leu Lys His His
65          70          75          80
Leu Gly Glu Ala Val Thr Gly Leu Leu Leu Ile Tyr Pro Thr Ser Ile
          85          90          95
Leu His Ile Leu Glu Ser Ser Ser Asp Thr Leu Tyr Lys Val Leu Leu
          100         105         110
Asp Tyr Ile Gly His Val Lys Asp Glu Thr Val Phe Phe Ile Gln Gln
          115         120         125
Met Lys Ile Ile Val Ile Ser His Asn Ile Pro Met Arg Leu Phe Met
          130         135         140
Gln Trp His Val Ser Val Ile Lys Val Pro Val Met Tyr Leu Asp Asp
          145         150         155         160
Val Thr Gln Ser Gln Ser Leu Lys Glu Val Ile Thr Asp Phe Leu Thr
          165         170         175
Gln Thr His Lys Leu Ser Leu Tyr Leu Cys Gln Thr Met Lys Val Gly
          180         185         190
Thr Lys Gly Pro Gly Asp Asn Leu His Gln Val Ala Pro Asp Leu Leu
          195         200         205
Leu Pro Glu Gln Ile Ile Lys Tyr Leu Cys Lys Ser Glu Glu Phe Met
          210         215         220
Asp Pro Ala Thr Phe Ile Asn Met Tyr Asn Arg Pro Ile His Ile Thr
          225         230         235         240
Leu Asp Ser Glu Val Val Trp Pro Ala Pro Ser Arg Phe Ala Leu Glu
          245         250         255
Tyr Met Pro Met Glu
          260

```

<210> 24

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Sequence ZC29127

<400> 24

cgtatcggcc ggccaccatg tccttttcgg tc

32

<210> 25

<211> 32

<212> DNA

$\langle 220 \rangle$

<400> 25

32